# Knowing Left from Right

**Submission No:**

1789

**Submission Type:**

Abstract Submission

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**Introduction:**

A principal motivation for the NIFTI file standard was its strict inclusion of orientation and location of datasets. Still, in recent years, the AFNI software group and users in the research community have discovered a number of important errors in well-known databases. In this work, we present a method for finding problems in left and right determinations.

The brain is a largely symmetric organ; however, in humans especially, the asymmetry is often a subject of research. It is troubling then to find that the left and right are often confused in practice. Without predetermined landmarks such as fiducial markers or known lesions, it is difficult to visually determine for any individual that a particular feature should be found on the left or right. However in the case of two imaging modalities as in FMRI with both EPI and T1-weighted anatomical datasets, we can determine a mismatch between the two modalities.

**Methods:**

The method presented here uses alignment to determine if the original or left-right flipped T1 image aligns better with the EPI dataset. The same cost function is used for alignment and the resulting costs are compared. For our typical processing pipeline, that cost metric is typically the local Pearson correlation. Our implementation includes the -check_flip option for align_epi_anat.py to do this check. A warning is presented to the user if the flip produces a better alignment than the original.

**Results:**

Using this straightforward method, left-right flips have been found in at least three sites' datasets of the Functional Connectome 1000, OpenFMRI and ABIDE databases. Surprisingly, all these were well-vetted by their experienced contributors and database administrators. One might wonder how this problem came about and how we can avoid this kind of problem in the future.

Datasets can have incorrect or missing information for several reasons. DICOM data from scanners can be wrong or ambiguous. Siemens, for example, uses a mosaic format that can have its slices stacked in reverse order. While that is documented in the header, it is a non-standard part of DICOM that various DICOM conversion tools may not follow. PACS systems and custom Matlab scripts by individual researchers can also mangle headers. In some cases we have seen, existing pipelines at various sites will use the older Analyze format that is missing any orientation information. While NIFTI format has a stricter definition included for orientation, even software that reads and writes NIFTI may make assumptions about orientation. All these dataset conversion tools can lead to errors in left-right flipping.

The left-right issue is overlooked because of a number of issues. First, the problem is not obvious visually. While mistakes in anterior-posterior and inferior-superior directions are obvious, left-right flips are much harder to detect, yet with good visualization tools, researchers can potentially find a discordance between two datasets. The afni GUI provides a number of tools to check for alignment, including edge enhanced display and overlay transparency, and these tools led to the initial discovery of this issue.

Secondly, many software packages do not include a check for a common orientation across datasets, so if a dataset arrives with no or incorrect orientation information in its header, it will often be ignored. In some cases, the orientation of only the first dataset or a specific orientation is assumed. In contrast, the AFNI software package will usually not proceed in cases where a common orientation

is required, or it will handle differences automatically . This issue became more evident with the recent evaluation of pipelines across software packages.
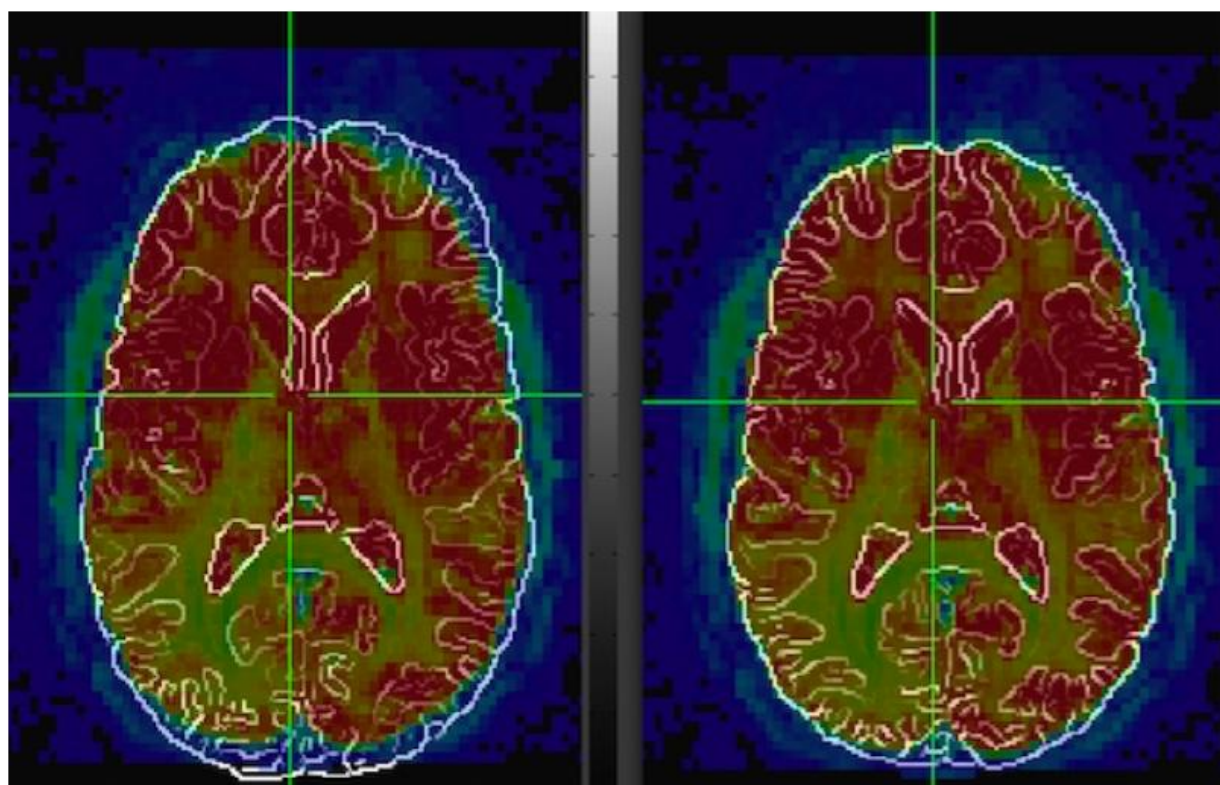


·Data flipping check. EPI data over anatomical edges. Original and flipped data shown to check for L-R errors.

**Conclusions:**

Here we present simple software solutions to evaluate this all-too-common problem. If possible, researchers should include a marker in scans (Vitamin-E capsule). Barring that, we emphasize users look closely at their data, and software developers put appropriate checks to detect mismatches.

**Imaging Methods:**

Anatomical MRI
BOLD fMRI [2]

**Informatics:**

Workflows

**Modeling and Analysis Methods:**

Image Registration and Computational Anatomy [1]
Methods Development

**Keywords:**

Data analysis
Data Organization
Data Registration
Other - symmetry asymmetry left right quality control

[1,2]Indicates the priority used for review

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**Please indicate which methods were used in your research:**

Functional MRI
Structural MRI

**For human MRI, what field strength scanner do you use?**

3.0T

**Which processing packages did you use for your study?**

AFNI

**Provide references using author date format**

Pauli R (2016), Exploring fMRI Results Space: 31 Variants of an fMRI Analysis in AFNI, FSL, and SPM. Frontiers in Neuroinformatics. 2016;10:24. doi:10.3389/fninf.2016.00024.

Bharat B. Biswal (2010), Toward discovery science of human brain function
PNAS 2010 107 (10) 4734-4739.

Di Martino, A. (2017), Enhancing studies of the connectome in autism using the autism brain imaging data exchange II.
Sci Data. 2017 March 14;4:170010.

ZS Saad (2009), A new method for improving functional-to-structural alignment using local Pearson correlation. NeuroImage, 44:839-848.

A. Andics (2017), Erratum for the Report "Neural mechanisms for lexical processing in dogs", Science 07 APR.

http://blogs.discovermagazine.com/neuroskeptic/2017/04/07/dogs-dont-language-left-brains